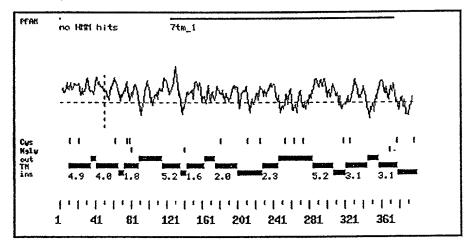
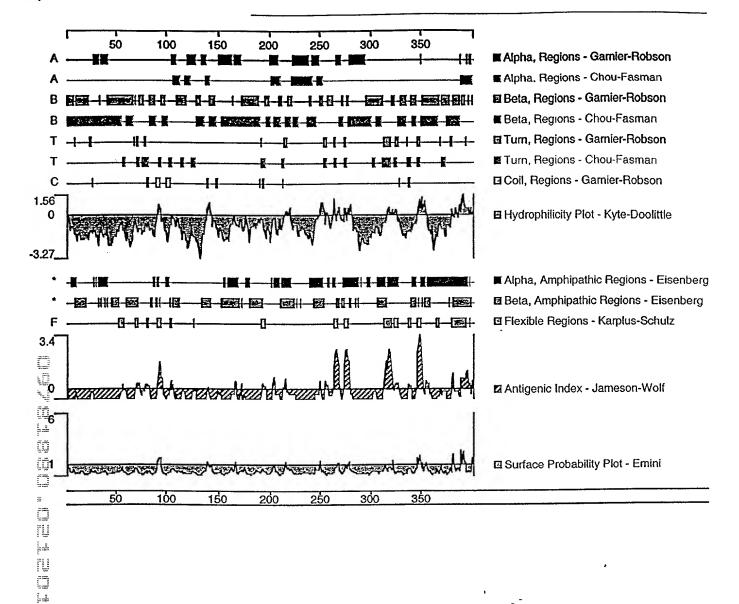
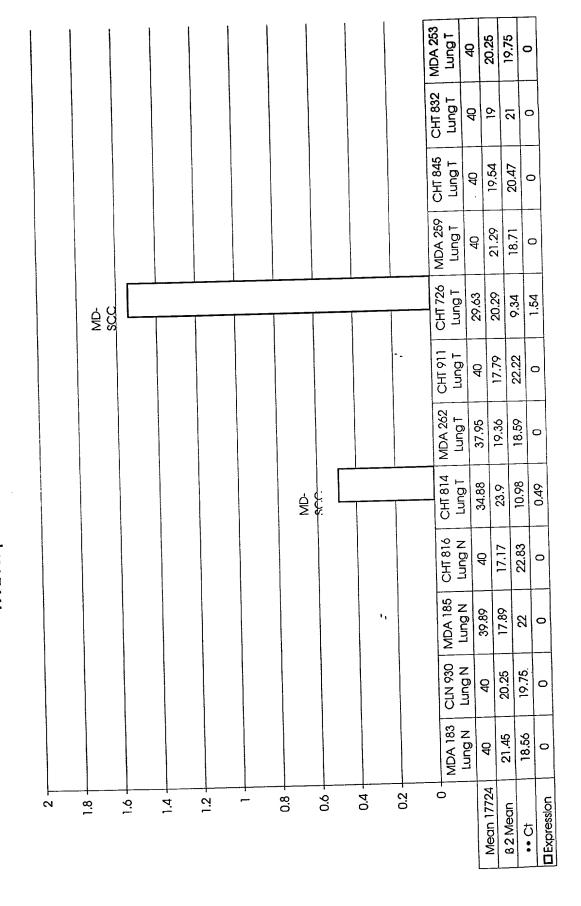
Analysis of 17724 (399 aa)



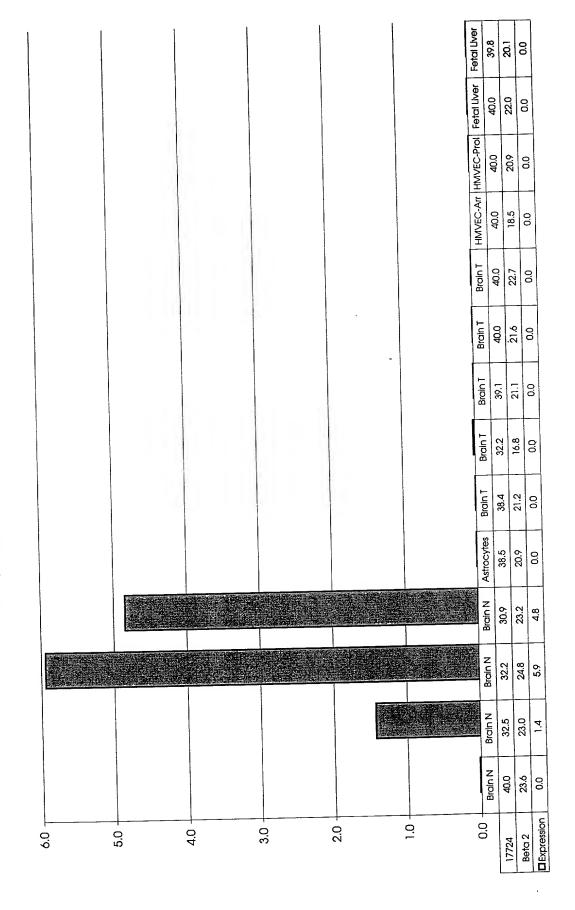


Query: 17724 Scores for sequence family classification (score includes all domains): Score E-value N Description 94.1 6.1e-29 1 7 transmembrane receptor (rhodopsin family) 7tm 1 Parsed for domains: score E-value Domain seq-f seq-t hmm-f hmm-t 1 259 [] 125 374 .. 94.1 6.1e-29 7tm_1 1/1 Alignments of top-scoring domains: Alignments of top-scoring domains: 7tm_1: domain 1 of 1, from 125 to 374: score 94.1, E = 6.1e-29 *->CN1LVilvilrtkklrtptnifilNLAvADLLflltlppwalyylvg GN ++i+ ++ +1+tp+++f++N ++ +L++ t +p +l+ 1+ 17724 125 GNTIIVMVIADTHLHTPMYFFLGNFSLLEILVTMTAVFRMLSDLLV 171 ${\tt gsedWpfGsalCklvtaldvvnmyaSillLtalSiDRYlAIvhPlryrrr}$ ++++ +C ++ ++ + + + + S 1 Lt +++DR++AI+hPlry ++ 172 --PHKVITFTGCMVQFYFHFSLGSTSFLILTDMALDRFVAICHPLRYGTL 219 17724 rtsprrAkvvillvWvlalllslPpllfswvktveegngtlnvnvtvCli ++ + ++ +++W++ +1+ +P ++s ++ + +g+ +n+++C+ 220 MS-RAMCVQLAGAAWAAPFLAMVPT-VLSRAHLDYCHGGV--INHFFCDN 265 17724 ${\tt dfpeestasvstwlrsyvllstlvgFllPllvilvcYtrIlrtlr}.....$ + ++s+ 1+++++1 1+1 +1v 1+ Y+ I+ t+ +++ 266 EPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLripsa 315 17724 ...kaaktllvvvvvFvlCWlPyfivllldtlc.lsiimsstCelervlp ++ + a+ ++ +++ v+ + i+l++++ + 5 ++ 316 sscQKAFSTCGSHLTLVFIGYSSTIFLYVRPGKaHS-------VQ 353 17724 tallvtlwLayvNsclNPiIY<-* + v+1+ +++ + 1NP+I 354 VRKVVALVTSVLTPFLNPFIL 17724

17724 Expression in Clinical Lung Samples



17724 Expression in Clinical Angiogenic Samples



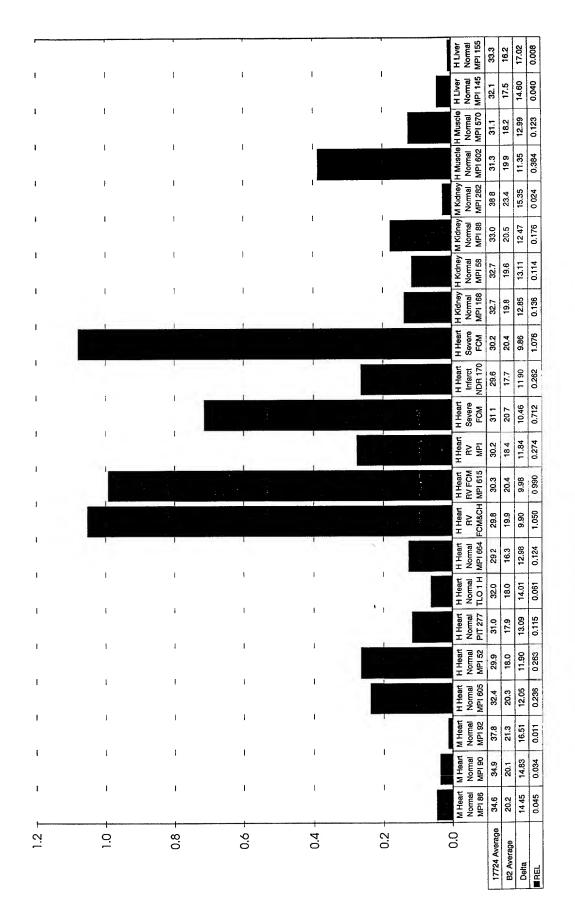


FIG. 6

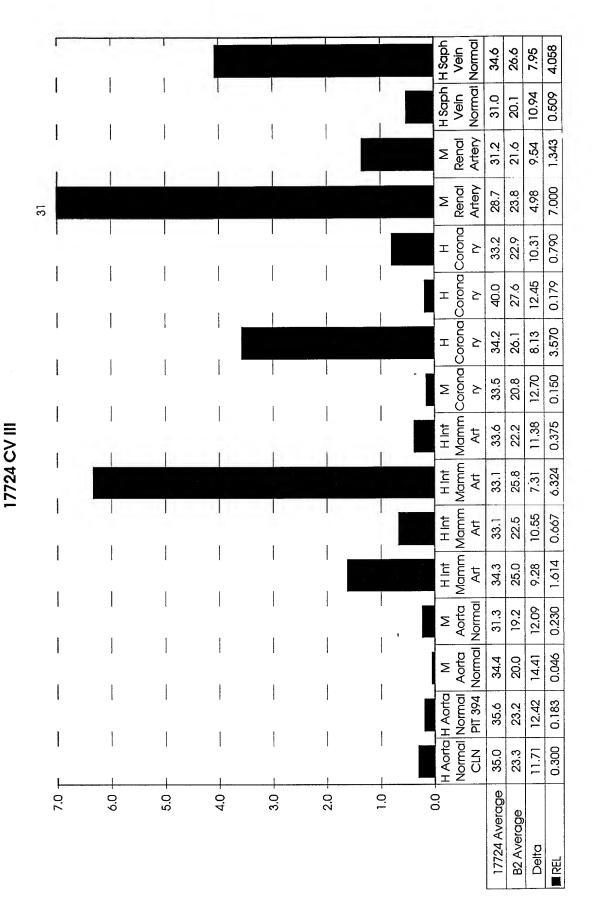


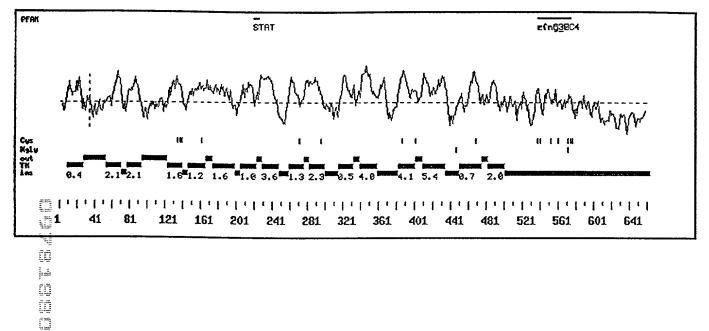
FIG. 7

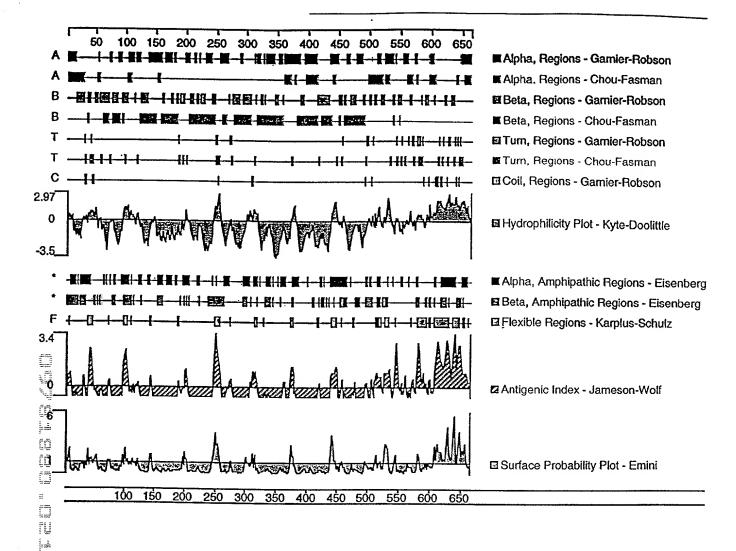
Phase 1.2.1 expression of 17724



Analysis of 31945

(663 aa)





GPCR 31945 Expression

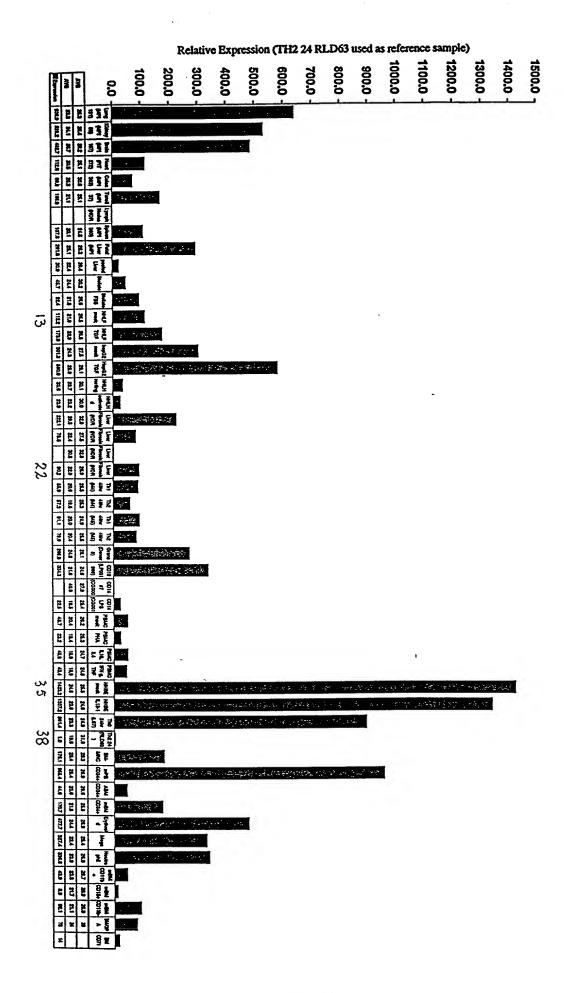
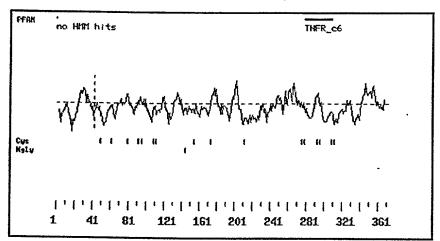
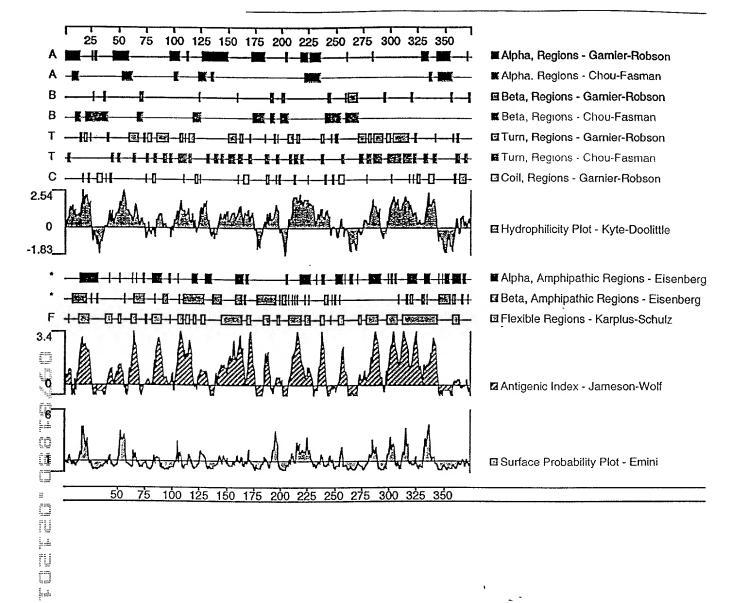
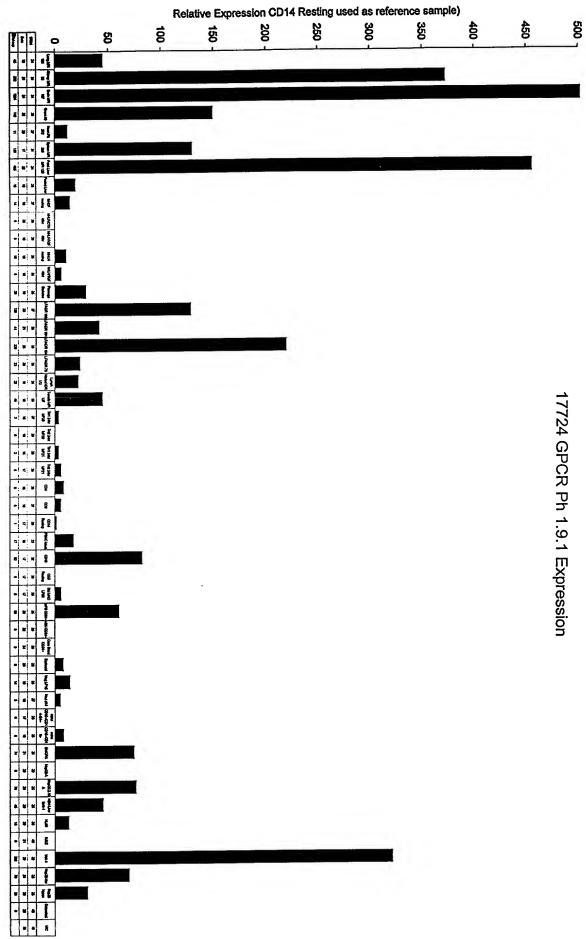


FIG. 11

Analysis of 50288 (372 aa)







Taqman Chart+Table

FIG. 14

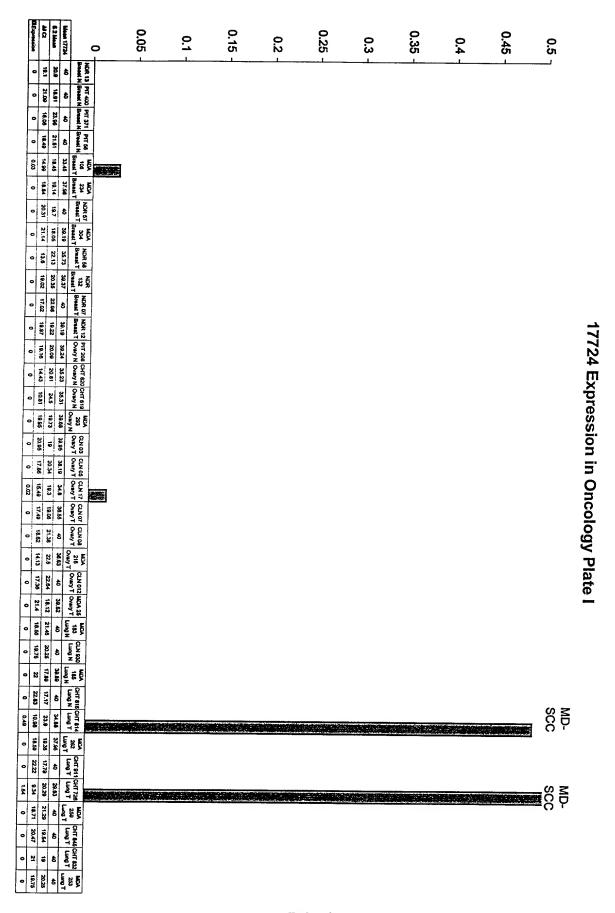


FIG. 15

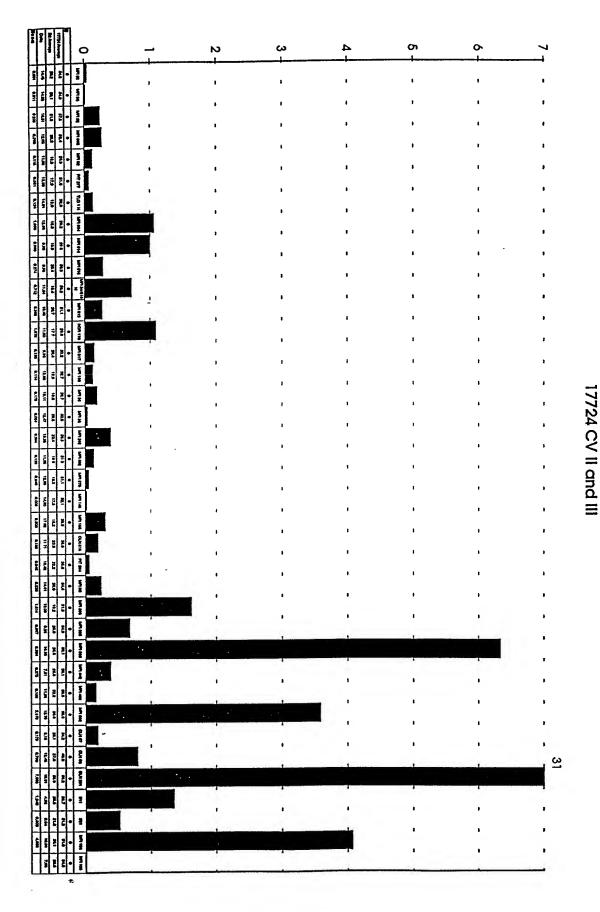


FIG. 16

Clone cbhTb018f11jt

